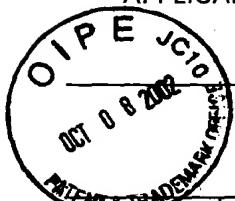


FORM PTO-1449 (Modified)

ATTY. DOCKET NO.
24737-1906CSERIAL NO.
09/709,905LIST OF PATENTS AND PUBLICATIONS FOR
APPLICANT'S INFORMATION DISCLOSURE
STATEMENTAPPLICANT
Ramnarayan et al.FILING DATE
November 10, 2000GROUP
1631

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE
NONE							

FOREIGN PATENT DOCUMENTS

		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes	No
NONE								

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

<i>JLB</i>	A	Koehl <i>et al.</i> , "A brighter future for protein structure prediction", <i>Nature Structure Biology</i> , 6(2):108-111, 1999
<i>JLB</i>	B	Sternberg <i>et al.</i> , "Progress in protein structure prediction: assessment of CASP3", <i>Current Opinion in Structural Biology</i> , 9:368-373, 1999

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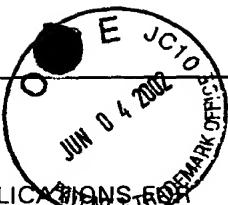
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FOREIGN PATENT DOCUMENTS

		DOCUMENT NUMBER								DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes	No
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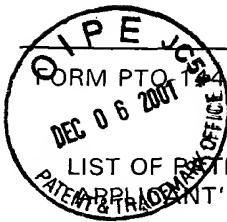
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EXAMINER INITIAL		DOCUMENT NUMBER								DATE	NAME	CLASS	SUB CLASS	FILING DATE
<i>JBS</i>	A	5	3	3	1	5	7	3	07/19/94	Balaji et al.				

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<i>JBS</i>	D	9	8	0	6	0	4	8	02/12/98	PCT				
<i>JBS</i>	E	9	8	1	3	7	8	1	04/02/98	PCT				
<i>JBS</i>	F	9	8	5	4	6	6	5	12/03/98	PCT				

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<i>JBS</i>	G	Abdel-Meguid, S.S. et al. "An orally bioavailable HIV-1 protease inhibitor containing an imidazole-derived peptide bond replacement: crystallographic and pharmacokinetic analysis," <i>Biochemistry</i> 33(39):11671-11677 (1994)
	H	Blaney, R. "Molecular modelling in the pharmaceutical industry. <i>Chemistry and Industry. Chemistry and Industry Review</i> 23(4):791-4 (1990). <i>not considered no copy provided</i>
	I	Bohm, G. "New approaches in molecular structure prediction". <i>Biophysical Chemistry</i> 59:1-32 (1996) <i>not considered no copy provided</i>
<i>JBS</i>	J	Thompson, S.K. et al. "Rational design, synthesis, and crystallographic analysis of a hydroxyethylene-based HIV-1 protease inhibitor containing a heterocyclic P1'-P2' amide bond isoster," <i>Journal of Medicinal Chemistry</i> 37(19):3100-3107 (1994).

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LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT		APPLICANT Ramnarayan et al.	TECH CENTER 1600/2900 RECEIVED AUG 14 2002
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U.S. PATENT DOCUMENTS

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* <i>JB</i>	AA	5	3	1	7	0	9	7	05/31/94	Miller et al.	536	24.31	10/07/91
* <i>JB</i>	AB	5	4	9	5	4	2	3	02/27/96	DeLisi et al.	364	496	10/25/93
* <i>JB</i>	AC	5	5	9	3	9	5	9	01/14/97	Miller et al.	514	8	10/14/93
* <i>JB</i>	AD	5	6	2	4	8	1	7	04/29/97	Miller et al.	435	69.1	04/28/94
* <i>JB</i>	AE	5	6	9	9	2	6	8	12/16/97	Schmidt	364	496	06/07/95
* <i>JB</i>	AF	5	9	6	8	7	3	7	10/19/99	Ali-Osman et al.	435	6	11/12/96
* <i>JB</i>	AG	5	9	7	8	7	4	0	11/02/99	Armistead et al.	702	19	08/09/95
* <i>JB</i>	AH	6	1	2	8	5	8	2	10/03/00	Wilson et al.	702	27	04/30/96

FOREIGN PATENT DOCUMENTS

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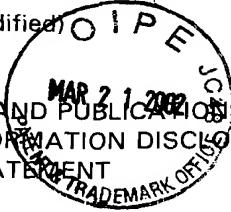
OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

* <i>JB</i>	AI	Baker et al., "Protein Structure Prediction and Structural Genomics", <i>Science</i> , 294:93-96 (2001)
* <i>JB</i>	AJ	Hess et al., "Impact of Pharmacogenomics on the Clinical Laboratory", <i>Mol. Diagn.</i> , 4(4):289-98 (1999)
* <i>JB</i>	AK	Hess et al., "Gene Therapy Monitoring: Clinical Monitoring for Efficacy and Potential Toxicity", <i>Mol. Diagn.</i> , 2(2):147-155 (1997)

EXAMINER <i>JB. Brusca</i>	DATE CONSIDERED <i>11/27/02</i>
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FORM PTO-1449 (Modified)  LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT	ATTY. DOCKET NO. 24737-1906C	SERIAL NO. 09/709,905
	APPLICANT Ramnarayan et al.	
	FILING DATE November 10, 2000	GROUP 1631
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* References are not included.

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER							DATE	NAME	CLASS	SUB CLASS	FILING DATE
*	AA	5	7	1	2	1	4	5	01/27/98	Houghton et al.	435	219	09/06/96

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		DOCUMENT NUMBER							DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes No

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*	AB	Ajay et al., Computational Methods to Predict Binding Free Energy in Ligand-Receptor Complexes, <u>Journal of Medicinal Chemistry</u> , 38(26):4953-4967 (1995). <i>Optical</i>
*	AC	Balaji et al., Conformational studies on model peptides with 1-aminocyclopropane 1-carboxylic acid residues, <u>Pept. Res.</u> , 7(2):60-71 (1994).
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*	AE	Balasubramaniam et al., [D-TRP ³²]Neuropeptide Y: A Competitive Antagonist of NPY in Rat Hypothalamus, <u>J. Med. Chem.</u> , 37(6):811-815 (1994).
*	AF	Böhm, Prediction of binding constants of protein ligands: A fast method for the prioritization of hits obtained from de novo design or 3D database search programs, <u>Journal of Computer-Aided Molecular Design</u> , 12:309-323 (1998).
*	AG	Checa et al., Assessment of Solvation Effects on Calculated Binding Affinity Differences: Trypsin Inhibition by Flavonoids as a Model System for Congeneric Series, <u>J. Med. Chem.</u> , 40:4136-4145 (1997).
*	AH	Daniels, Blood group polymorphisms: molecular approach and biological significance, <u>Transfus. Clin. Biol.</u> , 4:383-390 (1997) ✓

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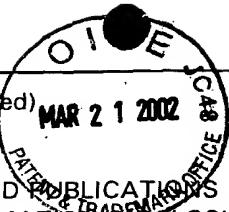
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	FILING DATE November 10, 2000	GROUP 1631

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*	AI	Das et al., Crystal Structures of 8-CI and 9-CI Complexed with Wild-type HIV-1 RT and 8-CI TIBO Complexed with the Tyr ¹⁸¹ Cys HIV-1 RT Drug-resistant Mutant, <u>J. Mol. Biol.</u> 264:1085-1100 (1996).
*	AJ	Eldridge et al., Empirical scoring functions: I. The development of a fast empirical scoring function to estimate the binding affinity of ligands in receptor complexes, <u>Journal of Computer-Aided Molecular Design</u> . 11:425-445 (1997).
*	AK	Fox, S. Pharmacogenomics Thrives in Europe. <u>Genetic Engineering News</u> , June 15, 1999.
*	AL	Leheny et al. Symposium on Resistance Highlights New Trends in AIDS Treatments: Implications for BioChem Pharma and Others, Hambrecht & Quist LLC Institutional Research, pp. 1-7 (1997). <i>not considered</i> no copy provided
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*	AN	Munson et al., Identification of an extracytoplasmic region of H+, K(+)- ATPase labeled by a K(+) -competitive photoaffinity inhibitor, <u>J. Biol. Chem.</u> 266(28):18976-88 (1991).
*	AO	Novotny et al., Empirical Free Energy Calculations: A Blind Test and Further Improvements to the Method, <u>J. Mol. Biol.</u> 268:401-411 (1997).
*	AP	Press Release, Structural Bioinformatics Inc. and Cyberchemics, Inc. Collaborate to Speed the Generation of Hepatitis C Viral Protease Inhibitors, <u>SBI News</u> . Located at http://strubix.com/press/press5.html , pp. 1-2 (1997).
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*	AR	Press Release, SBI Protein Models & Ligand Binding for Novel Viral Enzyme Validated, <u>SBI News</u> . Located at http://strubix.com/press/press32.html , pp. 1-2 (1999).
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*	AT	Press Release, SBI's Protein Structure Directed Combinatorial Chemistry Cuts Time and Cost 100X for Synthesis of New Anti-Inflammatory Drug Lead Molecules (TNF Receptor Antagonists), <u>SBI News</u> . Located at http://strubix.com/press/press19.html , pp. 1-2 (1998).

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*J.P. Bruce*DATE CONSIDERED *11/27/02*

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FORM PTO-1449 (Modified)		ATTY. DOCKET NO. 24737-1906C	SERIAL NO. 09/709,905
LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT		APPLICANT Ramnarayan et al.	
		FILING DATE November 10, 2000	GROUP 1631
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*	BA	Ramnarayan et al., Characterization of a Linear Pentapeptide Containing Two Consecutive β -Turns, <u>Pept. Res.</u> 7(5):270-8 (1994).
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*	BD	Shafer et al., Multiple Concurrent Reverse Transcriptase and Protease Mutations and Multidrug Resistance of HIV-1 Isolates from Heavily Treated Patients, <u>Annals of Internal Medicine</u> , 128(11):906-11 (1998).
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*	BF	Shenderovich et al., "Structural Pharmacogenetic Approach-to-the-Evaluation of Drug Resistant Mutations and HIV-1 Protease", <u>Journal of Clinical Ligand Assay</u> , 24(2):140-144 (2001) <i>not considered</i> <i>copy provided</i>

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LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT		
	APPLICANT Ramnarayan et al.	
	FILING DATE November 10, 2000	GROUP 1631

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

*	BG	Smith et al., Molecular modeling of HIV-1 reverse transcriptase drug-resistant mutant strains: implications for the mechanism of polymerase action, <u>Protein Engineering</u> , 10(12):1379-83 (1997). <i>copy provided</i>
*	BH	Spear, Viewpoint - Pharmacogenomics: Today, Tomorrow, and Beyond, <u>Drug Benefit Trends</u> , 11(2):53-54 (1999).
*	BI	Takamatsu et al., A New Method for Predicting Binding Free Energy Between Receptor and Ligand, <u>Proteins: Structure, Function, and Genetics</u> , 33:62-73 (1998).
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*	BM	Weng et al., Prediction of protein complexes using empirical free energy functions, <u>Protein Science</u> , 5:614-626 (1996). <i>not considered no copy provided</i>
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*	BO	Zhu et al., Analysis of high-affinity binding determinants in the receptor binding epitope of basic fibroblast growth factor, <u>Protein Eng.</u> , 10(4):417-21 (1997). <i>copy provided</i>
*	BP	Zhu et al., Glu-96 of basic fibroblast growth factor is essential for high affinity receptor binding. Identification by structure-based site-directed mutagenesis, <u>J. Biol. Chem.</u> , 270(37):21869-74 (1995). <i>copy provided</i>

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JRB. Brusca

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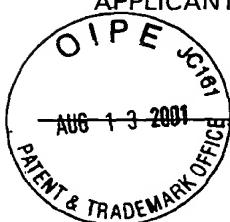
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Ramnarayan et al.

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EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE

FOREIGN PATENT DOCUMENTS

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LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT		APPLICANT Ramnarayan et al.	
		FILING DATE November 10, 2000	GROUP 2857 1631



U.S. PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NUMBER							DATE	NAME	CLASS	SUB CLASS	FILING DATE
*	4	2	0	8	4	7	9	06/17/80	Zuk et al.	435	7	07/14/77
*	4	2	2	0	4	5	0	09/02/80	Maggio	23	230	04/05/78
*	4	2	3	3	4	0	1	11/11/80	Yoshida et al.	435	7	07/14/77
*	4	2	3	3	4	0	2	11/11/80	Maggio et al.	435	7	04/05/78
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*	5	3	3	1	5	7	3	07/19/94	Balaji et al.	364	500	12/14/90
*	5	5	7	1	8	2	1	11/05/96	Chan et al.	514	312	05/20/94
*	5	5	7	9	2	5	0	11/26/96	Balaji et al.	364	496	04/24/95
*	5	6	1	2	8	9	5	03/18/97	Balaji et al.	364	496	04/21/95
*	5	7	1	2	1	4	5	01/27/98	Houghton et al.	435	219	09/06/96
*	5	8	0	8	9	6	9	09/15/98	Arnaud et al.	367	103	12/04/95
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*	5	8	4	6	7	6	3	12/08/98	Lee et al.	435	69.1	05/13/94
*	5	9	1	0	4	7	8	06/08/99	Hlavka et al.	514	9	09/20/96

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P	ENT & TRADE	DOCUMENT NUMBER							DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes No
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*	JBB	9	7	2	7	4	8	0	07/31/97	PCT			
*	JBB	9	9	0	6	5	9	7	02/11/99	PCT			

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John B. Brusca

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FORM PTO-1449 (Modified)		ATTY. DOCKET NO. 24737-1906C	SERIAL NO. 09/709,905
LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT		APPLICANT Ramnarayan <i>et al.</i>	
		FILING DATE November 10, 2000	GROUP 2857/631

O I P R S E C T I O N
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OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

* <i>JB</i>	Vajda <i>et al.</i> Empirical potentials and functions for protein folding and binding, <u>Theory and Simulation</u> . 7:222-228 (1997).
* <i>JB</i>	Vriend, G., WHAT IF: A molecular modelling and drug design program, <u>J. Mol. Graphics</u> 8:52-6 (1990).
* <i>JB</i>	Wang <i>et al.</i> , Calculation of Relative Binding Free energies and Configurational Entropies: A Structural and Thermodynamic Analysis of the Nature of Non-polar Binding of Thrombin Inhibitors Based on Hirudin ⁵⁵⁻⁶⁵ , <u>J. Mol. Biol.</u> 253:473-492 (1995).
* <i>JB</i>	Wang <i>et al.</i> , Analysis of Thermodynamic Determinants in Helix Propensities of Nonpolar Amino Acids through a Novel Free Energy Calculation, <u>J. Am. Chem. Soc.</u> 118:995-1001 (1996).
* <i>JB</i>	Wang <i>et al.</i> , Toward Designing Drug-Like Libraries: A Novel Computational Approach for Prediction of Drug Feasibility of Compounds, <u>J. Comb. Chem.</u> 1:524-33 (1999).
* <i>JB</i>	Weiner <i>et al.</i> An All Atom Force Field for Simulations of Proteins and Nucleic Acids, <u>Journal of Computational Chemistry</u> 7(2): 230-52 (1986).
*	Weng <i>et al.</i> , Prediction of protein complexes using empirical free energy functions, <u>Protein Science</u> . 5:614-626 (1996). <i>not considered in claim prioritized</i>
* <i>JB</i>	Yan <i>et al.</i> , Complex of NS3 protease and NS4A peptide of BK strain hepatitis C virus: A 2.2 Å resolution structure in a hexagonal crystal form, <u>Protein Science</u> 7:837-847 (1998).
* <i>JB</i>	Zhou <i>et al.</i> How and why phosphotyrosine-containing peptides bind to the SH2 and PTB domains, <u>Folding & Design</u> . 3(6):513-522 (1998).
* <i>JB</i>	Zhu <i>et al.</i> , Identification of two new hydrophobic residues on basic fibroblast growth factor important for fibroblast growth factor receptor binding, <u>Protein Engineering</u> 11(10):937-40 (1998).
* <i>JB</i>	Zhu <i>et al.</i> , Analysis of high-affinity binding determinants in the receptor binding epitope of basic fibroblast growth factor, <u>Protein Eng.</u> 10(4):417-21 (1997).
* <i>JB</i>	Zhu <i>et al.</i> , Glu-96 of basic fibroblast growth factor is essential for high affinity receptor binding. Identification by structure-based site-directed mutagenesis, <u>J. Biol. Chem.</u> 270(37):21869-74 (1995).

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